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Application Serial Number: 09/830, 230

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FOR CRESUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER \$ 703 3 03 = 12 12.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX: 703-308-4216 PATENTIN 2.1 e-mail help: patin21help@uspto.gov.or phone;703-306-4119 (RsWax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax Park the Park of the Control of the

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## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address http://www.uspto.gov/web/offices/pac/checker

PCT

RAW SEQUENCE LISTING DATE: 05/08/2001 PATENT APPLICATION: US/09/830,230 TIME: 12:00:30

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Does Not Comply
Corrected Diskette Needed

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## ERRORED SEQUENCES

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302					165					170					175	
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323	G1	<b>3</b>	275	T	Db -	Dh.	<b>.</b>	280	C	T	G1	T	285	D	<b>3</b>	T
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326	<b>a</b> 1	290	<b>.</b>	17- 1	Db -		295	17- 1	m	<b>7</b>	Dh.	300	3	T	C	0
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	305	<b>a</b> 1		α.		310		•	<b>51.</b> .	•	315		<b>a</b>	**- 1	<b></b>	320
	ser	GIU	Asp	ser		Pne	Leu	Asp	Phe	_	Pne	ASI	ser	vai	_	ASII
332	_	<b>a</b> 1	-		325		-1.			330	<b></b>	•	m 1		335	D1
	Ser	GTĀ	ьys		Pro	туг	116	Arg	Asn	GIY	туг	ьeu	Thr		Pne	Pne
335		<b>01</b>		340		D		**- 1	345	*		m	17-1	350	<b>.</b>	<b>-1</b> -
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338	<b>D</b> 1		355	m			• -	360	D	m	<b>G</b>	<b>a</b> 1	365	<b>3</b>	D1	
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341		370		m1.	•	<b>a</b> 1	375	D1	•	m 1		380	<b>01</b>		D1	<b>03</b>
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344		C1	Dha	m l	3	390	37 n 1	M	Com	M	395	C1++	C1	m	m	400
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347	Dha	<b>3</b>	7	3	405	T	T	C1 -		410	Dha	C	Dha	C	415	T
	Pne	ASP	ASII	_	Thr	Leu	гàг	GIII	Ser 425	Leu	Pne	ser	Pne	430	ASII	Leu
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353	ASII	гуѕ	435	ASP	Val	Pne	GIY	440	Glu	Val	PIO	Pile	445	TAT	Leu	Phe
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356	гуу	450	пуъ	1111	GIU	Pile	455	пеп	ser	ASP	HIG	460	FIIE	ser	vaı	Val
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	rne	TÀT	_	Arg	THE	Pne	ASII	_	Gly	ser	iie	ьeu	525	ığı	гуу	Leu
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135

520 Glu Tyr Ile Leu Asp Met Asp Thr Asn Glu Lys Leu Tyr Phe Tyr Gly

140

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518 130

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	145				_	150	_				155					160
523	Asn	Glu	Phe	Leu	Val	Asp	Phe	Asp	Ser		Asn	Phe	Leu	Leu		Asn
524				٠	165					170					175	
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530			195	0-1	-1-			200	-1-				205			
	T OIL	Glu		λ1 =	Dho	λla	Thr		Sor	Luc	Tlo	Pro		Dro	Туг	Tur
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533		210	<b>-</b> -	. 1 -		<b>.</b>		m		Ŧ	D		<b>6</b> 3	<b>3</b>	nh -	<b>a</b> 1
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		Asn	ser	Val	IAT		ser	GTA	цуѕ	цуѕ		TYL	TIE	Arg	ASII	
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	Tyr	Leu	Thr	Tyr		Phe	Ala	GIu	Asn		АТА	Pro	Ser	vaı		гàг
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	Pro	Phe	Arg	_	Leu	Pne	ьуs	Pne	_	Thr	GIU	Pne	Leu		ser	Asp
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584					485			- 4 -		490	_	_			495	
	Tla	Leu	λen	Фът		T.au	λen	λen	T.A.II		T.Ou	Ser	Dho	Luc		Sor
	116	пеа	нэр	500	цуз	пец	N311	กวน	505	GIY	пеп	Jei	1 116	510	Leu	Jer
587	C1	M**	C1		T a	M•••	17-1	T~		D~-	t	C1	T~		T~	X
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DATE: 05/08/2001

TIME: 12:00:30

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4891 <222> OFFICE (3) 4884 <211> LENGTH: 185 4891 <223> OTHER INFORMATION: n equals a,t,g, or c 4893 <220> FEATURE: pg 7-8 W--> 4894 <221> NAME/KEY misc feature 4895 <222> LOCATION: (19) 4896 <223> OTHER INFORMATION: n equals a,t,q, or c 4898 <220> FEATURE: W--> 4899 <221> NAME/KEY misc feature 4900 <222> LOCATION: (28) 4901 <223> OTHER INFORMATION: n equals a,t,g, or c 4903 <220> FEATURE: W--> 4904 <221> NAME/KEY: misc feature 4905 <222> LOCATION: (32) 4906 <223> OTHER INFORMATION: n equals a,t,g, or c 4908 <220> FEATURE: misc feature 4910 <222> LOCATION: (46) 4911 <223> OTHER INFORMATION: n equals a,t,q, or c 4913 <220> FEATURE:

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,230

W--> 4914 <221> NAME/KEY misc feature

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Input Set : N:\COPIES\EBONY\PB481USsl.txt
                       Output Set: N:\CRF3\05082001\I830230.raw
     4915 <222> LOCATION: (72)
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     4918 <220> FEATURE:
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     4920 <222> LOCATION: (79)
     4921 <223> OTHER INFORMATION: n equals a,t,g, or c
     .4923 <220> FEATURE:
W--> 4924 <221> NAME/KEY: misc/feature
      4925 <222> LOCATION: (90)
      4926 <223> OTHER INFORMATION: n equals a,t,g, or c
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W--> 4934 <221> NAME/KEY@ misc feature
     4935 <222> LOCATION: (II8)
     4936 <223> OTHER INFORMATION: n equals a,t,g, or c
     4938 <220> FEATURE:
W--> 4939 <221> NAME/KEY misc feature
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     4948 <220> FEATURE:
W--> 4949 <221> NAME/KEY misc feature
     4950 <222> LOCATION: (145)
     4951 <223> OTHER INFORMATION: n equals a,t,g, or c
     4953 <220> FEATURE:
W--> 4954 <221> NAME/KEY: misc feature
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     4961 <223> OTHER INFORMATION: n equals a,t,g, or c
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E--> 4965 ekyklifkmh vnillvrqni nigdlidtrn lyffktpekd gilsnieksk klyklainyy 120
E--> 4966 sealkyhkkl enyttvklem dgitnwedey hkislkelny ydiikkellr idetkaffeq 180
E--> 4967 gpňyy
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     14027 <211> LENGTH: 1119
     14028 <212> TYPE: PRT
                                    2P-11-12
     14029 <213> ORGANISM: Homo sapiens
                                                                                remaining deriver in
Le requerce bove
same enne)
     14031 <220> FEATURE:
     14032 <221> NAME/KEY: SITE
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,230

DATE: 05/08/2001

TIME: 12:00:31

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14039 <223> OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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14042 <221> NAME/KEY: SITE
14043 <222> LOCATION: (735)
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14046 <400> SEQUENCE: 320
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                  20
                                       2.5
14053 Lys Leu Asn Asp Lys Asn Arg Glu Ile Met Leu Asn Glu Val Lys Asn
              35
14056 Ser Val Ile Asp Arg Asn Tyr Lys Lys Ala Tyr Ser Val Ala Lys Leu
                               55
                                                   60
14059 Leu Gln Asp Lys Tyr Pro Gln Asn Glu Asp Ile Ala Met Leu Thr Asn
14060 65
                          70
                                               7.5
14062 Thr Leu Ala Glu Ile Ala Asn Ser Ser Pro Phe Glu Ser Lys Asp Leu
                       85
                                           90
14065 Gln Arg Asp Ser Ala Asn Gln Ile Leu Asp Lys Ile Lys Gly Gln Asp
                  100
                                      105
14068 Asn Thr Lys Thr Asn Val Asn Glu Asn Phe Asp Ile Ala Phe Asn Asn
             115
                                  120
14071 Arg Tyr Ile Lys Asp Ser Thr Ile Thr Glu Asn Tyr Ser Asp Arg Asn
                              135
                                                  140
14074 Asp Asp Val Gly Ile Glu Asp Glu Asp Ile Ser Glu Phe Lys Lys Ser
                        150
14077 Lys Ile Pro Glu Lys Ile Lys Pro Asn Thr Asn Pro Lys Glu Glu Asp
                     165
                                          170
14080 Gln Ile Ile Gln Ser Pro Asn Pro Lys Leu Ser Val Asn Asp Gln Lys
14081
                 180
                                      185
                                                          190
14083 Asn Leu Phe Asn Leu Glu Lys Leu Lys Lys Asn Leu Ser Gly Lys Ser
             195
                                  200
14086 Asn Ser Glu Asn Ile Leu Asn Asp Ser Gln Lys Ile Glu Asn Asp Lys
         210
                              215
                                                  220
14089 Gln Asn Thr Asn Leu Ser Lys Glu Lys Asn Ser Glu Asn Ile Leu Lys
                          230
                                              235
14092 Thr Pro Asp Asn Ser Lys Tyr Ser Asn Asn Asn Thr Thr Ser Leu
                     245
                                          250
14095 Lys Lys Ile Ser Ser Asn Ser Gln Lys Glu Ser Glu Leu Ser Pro Pro
                  260
                                      265
14098 Ser Gln Thr Ile Ile Gly Lys Ile Tyr Arg Pro Tyr Ser Tyr Leu Ile
             275
                                  280
14101 Lys Lys Glu Leu Tyr Glu Ile Leu Asp Asp Ile Asn Thr Gly Arg Val
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Input Set : N:\COPIES\EBONY\PB481USsl.txt
Output Set: N:\CRF3\05082001\I830230.raw

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14107			Phe	Gln	_		Asn	Glu	Leu			Asn	Ser	Lys		
14108					325					330					335	
14110	Glu	Ala	Ser		Leu	Leu	Leu	Thr			Lys	Lys	Asp		Glu	Pro
14111				340					345					350		
14113		Leu		Asn	Ile	Pro	Lys			Tyr	Lys	Lys		Ile	Phe	Gln
14114			355					360					365			
14116			Lys	Glu	Asp	Lys		Pro	Gln	Tyr	Leu		Asp	Leu	Lys	Ser
14117		370					375					380	_			
14119	_	Val	His	Ser	Ile	_	Pro	Ile	Asp	Leu		Asn	Thr	Lys	Ser	
14120					_	390	_	_			395	_	_	_	_	400
14122		GIn	Ala	TTE		Asp	Leu	Asn	GIu		Leu	ьys	Asn	Asn		Asn
14123		<b>31.</b>	<b>a</b> 1		405	T	m )	T	31.	410	31.	3	T	T1_	415	TT 4 ~
14125 14126	ASP	Ala	GIn	420	ser	ьys	Thr	ьeu	425	GIN	Ата	ASII	гуя	430	GIII	HIS
14128	Tou	Clii	7 02		T 17.0	Cor	Tvc	Wa 1		cor	T10	Tvc	Dro	+	7 cn	Lou
14129		GIU	435	Leu	гуз	ser	гуѕ	440	птэ	ser	11e	гуъ	445	116	АБР	пеп
14131		Δen		T.ve	ser	Δra	Gln		Δla	Tla	Luc	Δen		Δen	Glu	Dhe
14132	Olu	450	* ***	, J	501	**** 9	455	0	1114	110	27.5	460	ЦСИ	11011	OIU	1
14134	Leu		Asn	Asn	Pro	Asn		Ala	Gln	Ala	Ser		Thr	Leu	Ala	Gln
14135		-10				470			0		475	-1-				480
14137		Asn	Lys	Ile	Gln		Leu	Glu	Asp	Leu		Ser	Lys	Val	His	Ser
14138			•		485				-	490	•		-		495	
14140	Ile	Lys	Pro	Ile	Asp	Leu	Glu	Asn	Thr	Lys	Ser	Arg	Gln	Gln	Ala	Ile
14141				500					505	_				510		
14143	Lys	Asp	Leu	Asn	Glu	Phe	Leu	Lys	Asn	Asn	${\tt Pro}$	Asn	Asp	Ala	Gln	Ala
14144			515					520					525			
14146	Ser	Lys	Thr	Leu	Ala	Gln	Ala	Asn	Lys	Ile	Gln	His	Leu	Glu	Asp	Leu
14147		530					535					540				
14149		Ser	Lys	Val	His		Ile	Lys	Pro	Ile		Leu	Glu	Asn	Thr	
14150						550					555					560
14152	Ser	Arg	Gln	Gln		Ile	Lys	Asp	Leu		Glu	Phe	Xaa	Lys		Asn
14153	_		_		565	- 1	_	_		570				_	575	1
14155	Pro	Asn	Asp		GIn	Ala	Ser	Lys		Leu	Ala	GIn	Ala		Lys	Пе
14156	<b>C1</b> =	***	T	580	<b>3</b>	T	T	C	585	37- 1	***	C	T1 -	590	D	T1.
14158	GIN	HIS		GIU	Asp	Leu	гàг	Ser 600	ьуs	vaı	HIS	ser		гàг	Pro	ire
14159 14161	N a n	Lou	595	λan	Πhr	T	C0*		C12	Cla	212	Tlo	605	7.55	Lou	A con
14162	ASP	610	GIU	ASII	1111	тÃР	615	AIG	GIII	GIII	нта	620	тÃ2	ASP	neu	ASII
14164	G111		Yaa	T.ve	Acn	Δen		Acn	Aen	<b>Δ</b> 1 a	Gln		Sar	Tve	Thr	T.011
14165		rne	лаа	цуз	ASII	630	FIU	изп	изъ	та	635	AIG	Ser	цуз	1111	640
14167		Gln	Ala	Asn	Lvs		Gln	His	Leu	Glu		Leu	Lvs	Ser	Lvs	
14168					645					650			_, _		655	
14170	His	Ser	Ile	Lys		Ile	Asp	Leu	Glu		Thr	Lys	Ser	Arq		Gln
14171				660			<b>F</b> -		665			• -		670		
14173	Ala	Ile	Lys	Asp	Leu	Asn	Glu	Phe	Leu	Lys	Asn	Asn	Pro	Asn	Asp	Ala
14174			675					680					685			
14176	Gln	Ala	Ser	Lys	Thr	Leu	Ala	Gln	Ala	Asn	Lys	Ile	Gln	His	Leu	Glu

WOLL

	14177		690					695					700				
	14179	Asp	Leu	Lys	Ser	Lys	Val	His	Ser	Ile	Lys	Pro	Ile	Asp	Leu	Glu	Asn
- 1.0	14180						710					715					720
AK.	14182	Thr	Lys	Ser	Arg	Gln	Gln	Ala	Ile	Lys	Asp	Leu	Asn	Glu	Phe	Xaa	Lys
<b>U</b> ( <b>U</b> )	14183		-		•	725				-	730					735	_
	14185	Asn	Asn	Pro	Asn	Asp	Ala	Gln	Ala	Ser	Lys	Thr	Leu	Ala	Gln	Ala	Tyr
	14186				740	•				745	-				750		_
	14188	Glu	Asn	Asn	Gly	Asp	Leu	Leu	Lys	Ala	Glu	Asn	Ala	Tyr	Glu	Lys	Ile
	14189			755	-	-			760					765		-	
	14191	Ile	Lvs		Thr	Asn	Thr	Gln	Glu	Asp	His	Tyr	Lys	Leu	Gly	Ile	Ile
	14192		770					775		•		•	780		•		
	14194	Arq	Phe	Lys	Leu	Lvs	Lys	Tyr	Glu	His	Ser	Ile	Glu	Ser	Phe	Asp	Gln
	14195	_		-1 -		-1 -	7.90	-1-				795				•	800
	14197	Thr	Ile	Lys	Leu	Asp	Pro	Lys	His	Lys	Lys	Ala	Leu	His	Asn	Lys	Gly
	14198			•		805		•		•	810					815	•
	14200	Ile	Ala	Leu	Met	Met	Leu	Asn	Lvs	Asn	Lys	Lys	Ala	Ile	Glu	Ser	Phe
	14201				820				-1-	825					830		
	14203	Glu	Lvs	Ala	-	Gln	Ile	Asp	Lvs		Tyr	Gly	Thr	Ala	Tyr	Tyr	Gln
	14204			835					840		•	•		845	•	•	
	14206	Lvs	Glv		Ala	Glu	Glu	Lvs		Glv	Asp	Met	Gln	Gln	Ala	Phe	Ala
	14207		850					855	-	- 4	-		860				
	14209	Ser		Lvs	Asn	Ala	Tvr		Leu	Asp	Lvs	Asn	Pro	Asn	Tyr	Ala	Leu
	14210						870					875	_		-		880
	14212		Ala	Glv	Ile	Val		Asn	Asn	Leu	Glv		Phe	Lvs	Gln	Ser	Glu
	14213	-10		U-1		885					890			-1 -		895	
	14215	Glu	Tvr	Leu	Asn		Phe	Àsn	Ala	Asn		Lvs	Lvs	Pro	Asn		Ile
	14216		-1-		900					905					910		
	14218	Ala	Ile	Tvr		Leu	Ser	Ile	Ala		Phe	Glu	Asn	Asn	Lvs	Leu	Glu
	14219			915					920	-1-				925			
	14221	Glu	Ser		Glu	Thr	Ile	Asn		Ala	Ile	Asp	Leu	Asn	Pro	Glu	Lvs
	14222		930					935	-4-				940				_1 -
	14224	Ser		Tvr	Leu	Tvr	Leu		Ala	Ser	Ile	Asn		Lvs	Lvs	Glu	Asn
	14225			•		•	950	•				955		•	•		960
	14227	Tyr	Gln	Asn	Ala	Ile	Ser	Leu	Tvr	Ser	Leu	Val	Ile	Glu	Lys	Asn	Pro
	14228	-				965			-		970				-	975	
	14230	Glu	Asn	Thr	Ser	Ala	Tyr	Ile	Asn	Leu	Ala	Lys	Ala	Tyr	Glu	Lys	Ser
	14231				980		-			985		-		_	990	_	
	14233	Gly	Asn	Lys	Ser	Gln	Ala	Ile	Ser	Thr	Leu	Glu	Lys	Ile	Ile	Asn	Lys
	14234	-		995					.000				_	1005			-
	14236	Asn	Asn	Lys	Leu	Ala	Leu	Asn	Asn	Leu	Gly	Ile	Leu	Tyr	Lys	Lys	Glu
	14237		.010	-				015			_		1020	_	_	_	
	14239	Lys.	Asn	Tyr	Gln	Lys	Ala	Ile	Glu	Ile	Phe	Glu	Lys	Ala	Ile	Ile	Asn
:>	14240	025	<b>)</b> /0	25			.030					035	_				040
	14242	Ser	Asp	Ile	Glu	Ala	Lys	Tyr	Asn	Leu	Ala	Thr	Thr	Leu	Ile	Glu	Ile
	14243		•			1045	-	-			1050					.055	
	14245	Asn	Asp	Asn	Thr	Arg	Ala	Lys	Asp	Leu	Leu	Arg	Glu	Tyr	Thr	Lys	Leu
	14246		•		1060	-		-		.065		-			1070	-	
	14248	Lys	Pro			Pro	Glu	Ala			Ala	Leu	Gly	Ile	Ile	Glu	Tyr
	14249			.075					080				_	.085			

Input Set : N:\COPIES\EBONY\PB481USsl.txt
Output Set: N:\CRF3\05082001\I830230.raw

14251 Asn Glu Asn Asn Asn Asp Gln Thr Leu Arg Glu Leu Ile Lys Lys Phe 1090 1095 1100 14254 Pro Asn Tyr Lys Lys Asn Glu Asn Ile Lys Lys Ile Ile Gly Ile E--> 14255(105)/105 1110 14257 <210> SEQ ID NO: 321 14258 <211> LENGTH: 1087 14259 <212> TYPE: PRT 14260 <213> ORGANISM: Homo sapiens 14262 <220> FEATURE: 14263 <221> NAME/KEY: SITE 14264 <222> LOCATION: (541) 14265 <223> OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids 14267 <220> FEATURE: 14268 <221> NAME/KEY: SITE 14269 <222> LOCATION: (595) 14270 <223> OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids 14272 <220> FEATURE: 14273 <221> NAME/KEY: SITE 14274 <222> LOCATION: (703) 14275 <223> OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids 14277 <400> SEQUENCE: 321 14278 Lys Leu Asn Asp Lys Asn Arg Glu Ile Met Leu Asn Glu Val Lys Asn 14281 Ser Val Ile Asp Arg Asn Tyr Lys Lys Ala Tyr Ser Val Ala Lys Leu 20 25 14284 Leu Gln Asp Lys Tyr Pro Gln Asn Glu Asp Ile Ala Met Leu Thr Asn 35 40 14287 Thr Leu Ala Glu Ile Ala Asn Ser Ser Pro Phe Glu Ser Lys Asp Leu 14290 Gln Arg Asp Ser Ala Asn Gln Ile Leu Asp Lys Ile Lys Gly Gln Asp 70 14293 Asn Thr Lys Thr Asn Val Asn Glu Asn Phe Asp Ile Ala Phe Asn Asn 90 85 14296 Arg Tyr Ile Lys Asp Ser Thr Ile Thr Glu Asn Tyr Ser Asp Arg Asn 100 105 14299 Asp Asp Val Gly Ile Glu Asp Glu Asp Ile Ser Glu Phe Lys Lys Ser 115 120 14302 Lys Ile Pro Glu Lys Ile Lys Pro Asn Thr Asn Pro Lys Glu Glu Asp 130 135 140 14305 Gln Ile Ile Gln Ser Pro Asn Pro Lys Leu Ser Val Asn Asp Gln Lys 150 155 14308 Asn Leu Phe Asn Leu Glu Lys Leu Lys Lys Asn Leu Ser Gly Lys Ser 165 170 14311 Asn Ser Glu Asn Ile Leu Asn Asp Ser Gln Lys Ile Glu Asn Asp Lys 180 185 14314 Gln Asn Thr Asn Leu Ser Lys Glu Lys Asn Ser Glu Asn Ile Leu Lys 195 200 14317 Thr Pro Asp Asn Ser Lys Tyr Ser Asn Asn Asn Thr Thr Ser Leu

14320 14321	-	-	Ile	Ser	Ser	Asn 230	Ser	Gln	Lys	Glu	Ser 235	Glu	Leu	Ser	Pro	Pro 240
14321			Thr	Ile			Lys	Ile	Tyr			Tyr	Ser	Tyr		
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14326 14327		Lys	Glu	Leu 260	Tyr	Glu	Ile	Leu	Asp 265	Asp	Ile	Asn	Thr	Gly 270	Arg	Val
14329 14330		Leu	Gly 275	Lys	Asn	Arg	Leu	Lys 280	Glu	Leu	Ile	Lys	Lys 285	Gly	Leu	Ser
14330		Lvs		Gln	Lvs	Val	Asn		Leu	Tle	Glu	Asn		Lvs	Asn	Lvs
14333		290	1	0.2		,	295	014	200			300		-10		-1-
14335		Ala	Ser	Asn	Leu	Leu	Leu	Thr	Leu	Ile	Lys	Lys	Asp	Ile	Glu	Pro
14336						310					315					320
14338	Asn	Leu	Ile	Asn	Ile	Pro	Lys	Asp	${\tt Pro}$	Tyr	Lys	Lys	Glu	Ile	Phe	Gln
14339					325					330					335	
14341		Asp	Lys		Asp	Lys	Lys	Pro		Tyr	Leu	Glu	Asp		Lys	Ser
14342			_	340	_				345	_		_		350	_	
14344		Val		Ser	Ile	Lys	Pro		Asp	Leu	Glu	Asn		Lys	Ser	Arg
14345		<b>61</b>	355	<b>-1</b> -	<b>T</b>	<b>3</b>	<b>.</b>	360	<b>01</b>	Db -	T	T	365	3	D	7~~
14347 14348		370	Ата	rre	ьys	Asp	ьеu 375	ASII	GIU	Pne	Leu	380	ASII	ASII	PIO	ASII
14340			Cln	λla	Sar	Luc		T.011	Δla	Gln	Δla		Lve	Tle	Gln	ніс
14351		niu	GIII	nia	DCI	390		БСи	mu	0111	395	21011	270	110	<b>0</b> ±	400
14353		Glu	Asp	Leu	Lvs		Lvs	Val	His	Ser		Lvs	Pro	Ile	Asp	
14354		0_0			405		-1-			410		-1 -			415	
14356		Asn	Thr	Lys	Ser	Arg	Gln	Gln	Ala	Ile	Lys	Asp	Leu	Asn	Glu	Phe
14357				420		-			425		_	_		430		•
14359	Leu	Lys	Asn	Asn	Pro	Asn	Asp	Ala	Gln	Ala	Ser	Lys	Thr	Leu	Ala	Gln
14360			435					440					445			
14362	Ala	Asn	Lys	Ile	Gln	His		Glu	Asp	Leu	Lys		Lys	Val	His	Ser
14363		450					455				_	460				
14365		Lys	Pro				Glu	Asn	Thr	Lys		Arg	Gln	Gin	Ala	
14366		3	T			470	T 0	T	7 a n	7.00	475	7.00	Nan	7 1°a	C15	480
14368 14369	rys	ASP	Leu	ASII	485	Pne	Leu	гуу	ASII	490	PIO	ASII	ASP	Ald	495	Ala
14371	Sar	Luc	Thr			Gln	Δla	Δen	Lve		Gln	Hic	T.e.11	Glu		T.en
14372	JCI	כעם	1111	500	niu	01	mu	11011	505	110	01	******	200	510		
14374	Lvs	Ser	Lvs		His	Ser	Ile	Lys		Ile	Asp	Leu	Glu	-	Thr	Lys
14375			515					520			-		525			•
14377	Ser	Arg	Gln	Gln	Ala	Ile	Lys	Asp	Leu	Asn	Glu	Phe	Xaa	Lys	Asn	Asn
14378		530					535					540	f			
14380	Pro	Asn	Asp	Ala	Gln	Ala	Ser	Lys	Thr	Leu	Ala	Gln	Ala	Asn	Lys	Ile
14381						550					555					560
14383	Gln	His	Leu	Glu		Leu	Lys	Ser	Lys		His	Ser	Ile	Lys		Ile
14384		_		_	565	_	_	_		570			_	_	575	_
14386	Asp	Leu			Thr	Lys	Ser	Arg		GIn	Ala	ITe	Lys		Leu	Asn
14387		-1		580	<b>-</b>		D		585	27 -	a1	<b>31</b> -	0	590	m1	T
14389	GLU	rne		гаг	Asn	Asn	rro	<b>Asn</b> 600	Asp	ATG	GIN	нтα	605	гÀЗ	rnr	ren
14390 14392	Δla	Gln	595 Ala	Δen	T.v.e	Tle	Glr		T.eu	Glu	Asp	Len		Ser	Lve	Va 1
14372	nru	GIH	ara	A3II	- Y -	116	U = 11	****	<b></b> _u	JIU	٦.٥٢		-13		_, 5	

	•																
	14393		610					615					620				
	14395	His	Ser	Ile	Lys	Pro	Ile	Asp	Leu	Glu	Asn	Thr	Lys	Ser	Arg	Gln	Gln
	14396				-		630	_				635	_		-		640
	14398		Ile	Lvs	Asp	Leu	Asn	Glu	Phe	Leu	Lvs	Asn	Asn	Pro	Asn	Asp	Ala
	14399					645					650					655	
	14401	Gln	Ala	Ser	Lvs	Thr	Leu	Ala	Gln	Ala	Asn	Lvs	Ile	Gln	His	Leu	Glu
	14402	O		001	660	+			<b>V</b>	665		_1_			670		
	14404	Δen	T.e.ii	T.vc		Tue	Va 1	His	Ser		Lvs	Pro	Tle	Asn	•	Glu	Asn
	14405	1100		675	001	<b>1</b> 15			680					685		010	
w.C.W	14407	Thr	Lve		Ara	C1n	Gln	Δla		Tue	Δen	Τ.Δ11	Δen		Dho	Yaa	T.ve
" 0	14408	1111	690	SEI	птд	GIII	GIII	695	116	цуз	nsp	шец	700	GIU	THE	Auu	ц
	14410	λen		Dro	λen	Acn	λla		λla	Sor	Luc	Thr		λla	Gln	λla	mar
	14411		nou	FIU	Maii	нар	710	GIII	ALG	261	цуз	715	neu	ΑIα	GIII	ALG	720
	14411		A an	N an	C1**	) an		Lou	Tuc	λla	Clu		λla	Mirr	C1 <sub>11</sub>	Lvc	
		Gru	ASII	ASII	GIY	725	Leu	цец	цÃ2	MIG	730	ASII	ніа	TYL	GIU	735	116
	14414	T10	Tvva	T 0	mh∽		mbr	Cln	C1	λαη	-	m	Tvc	t ou	C1.,		т10
	14416		гуу	Leu	740	ASII	THI	GIII	Gru	745	птъ	тўт	гуъ	Leu	750	TIE	116
	14417		Dho	T G		T	T	Tr. xx	C1.,		cor	т1.	C1.,	Cor		λαn	Cln
	14419	Arg	Pne	755	Leu	гуу	гуу	ıyı	760	птъ	ser	ire	Gru	765	rne	ASP	GIII
	14420	mb~	Tlo		T 011	7 00	Dwo	T		T ++-	Trro	717	T 011		Nan	Tvva	C1 **
	14422	TIIL	770	гуѕ	neu	Asp	PIO	775	птъ	nys	пÃ2	Ата	780	птэ	ASII	гуу	GIY
	14423	т1.		т о	Wat	Wat	T 011		T	Nan	T	T		т1.	C1.,	C02	Dho
	14425		Ald	ьеu	Met	Mec	790	ASII	nys	ASII	цуз	795	нта	116	GIU	261	800
	14426 14428		Tura	7 l a	т1.	C12		7.00	T ***	N an	Птт∞		Пhх	λla	TTTT T	m	
	14429	GIU	гуѕ	нта	TIE	805	iie	ASP	гÃ2	ASII	810	GIŞ	1111	нта	TÄT	815	GIII
	14429	T 115	C1.,	Tla	λla		Clu	Tvc	λen	Clu		Mot	C1n	Gln	7 l s		λla
	14431	гуз	GLY		820	GIU	Giu	цуз	ASII	825	кар	Met	GIII	GIII	830	FIIC	AIG
	14434	Cor	Dho			λla	TT-7-	λcn	t ou		Tvc	λcn	Dro	Acn		λla	LOU
	14435	Ser	rne	835	VOII	AIG	1 7 1	ASII	840	АЗР	цуз	N311	110	845	ıyı	пта	пец
	14437	Tuc	λla		T10	Wa l	Sor	λen	-	Lou	Clv	λen	Dho		Gln	Sor	Glu
	14438	цуз	850	GIY	116	Val	261	855	ASII	Deu	GLY	nsii	860	цуз	GIII	Jer,	GIU
	14440	Glu		LOU	λen	Dha	Dha		Δla	λen	Δla	Luc		Dro	λen	Glu	Tla
	14441		TYT	ьеu	ASII	rne	870	N311	nia	N311	AIG	875	цуз	110	AJII	GIU	880
	14443		Tlo	Фил	λen	Lau		Tla	λla	Luc	Dho		λen	λen	T.ve	Lau	
	14444	niu	116	111	AJII	885	JCI	110	AIG	цуз	890	Olu	AJII	non	D <sub>f</sub> S	895	Olu
	14446	Glu	Sar	Len	Glu		Tla	Δen	Luc	Δla		Aen	T.211	Δen	Pro		Lve
	14447	GIU	261	пец	900	1111	116	non	цуэ	905	110	пэр	LCu	กรถ	910	Olu	цуз
	14449	Ser	Glu	Tur		Ψvr	T.Q11	Lve	Δla		Tle	Δsn	T.eu	Lvs		Glu	Δsn
	14450	ocı	Olu	915	ыси	- 7 -	LCu	<b>D</b> , 3	920	OCI	110	11511	шеш	925	<b>L</b> <sub>2</sub> 3	Oiu	
	14452	ጥህን	Gln	-	Δla	T1_	Ser	Leu		Ser	T.eu	Va 1	Tle		Lvs	Δen	Pro
	14453	- <u>y -</u>	930	non	niu	110	JCI	935	-1-	DCI	пси	141	940	Olu	11,5	11011	110
	14455	Glu		Thr	Ser	Δla	тur	-	Δsn	I.e.ii	Δla	Lvc		Tur	Glu	Lvc	Ser
	14456		*1511		001	1114	950			200		955		-1-			960
	14458		Agn	T.v e	Ser	Gln		Tle	Ser	Thr	Len		Lvs	Tle	Tle	Asn	
	14459	1		-, 0	JU1	965					970		_, _			975	_, _
	14461	Asn	Asn	Lve	Len		Len	Asn	Asn	Leu		Ile	Leu	Tvr	Lvs		Glu
	14462			_, 5	980		u			985	1			-1-	990	_, •	J_ u
	14464	Lvs	Asn	Tvr		Lvs	Ala	Tle	Glu		Phe	Glu	Lvs	Ala		Tle	Asn
	14465	_, 0		995	J-11	_, 5	-,		.000				_	.005			
								_					_				

Input Set : N:\COPIES\EBONY\PB481USs1.txt
Output Set: N:\CRF3\05082001\I830230.raw

14467 Ser Asp Ile Glu Ala Lys Tyr Asn Leu Ala Thr Thr Leu Ile Glu Ile 1010 1015 1020 14470 Asn Asp Asn Thr Arg Ala Lys Asp Leu Leu Arg Glu Tyr Thr Lys Leu E--> 14471025 /025 1030 103514473 Lys Pro Asn Asn Pro Glu Ala Leu His Ala Leu Gly Ile Ile Glu Tyr 1045 1050 14474 1055 14476 Asn Glu Asn Asn Asn Asp Gln Thr Leu Arg Glu Leu Ile Lys Lys Phe 14477 1060 1065 14479 Pro Asn Tyr Lys Lys Asn Glu Asn Ile Lys Lys Ile Ile Gly Ile 14480 1075 1080 16273 <210> SEQ ID NO: 364 16274 <211> LENGTH: 1036 16275 <212> TYPE: PRT 16276 <213> ORGANISM: Homo sapiens 16278 <400> SEQUENCE: 364 16279 Met Leu Val Lys Arg Ile Val Gly Lys Pro Ile Thr Met Leu Ile Leu 10 16282 Phe Ser Leu Leu Leu Met Ile Ser Leu Tyr Thr Phe Ser Arg Leu Lys 30 16283 20 . 25 16285 Val Asp Leu Leu Pro Gly Ile Asp Ile Pro Gln Ile Ser Ile His Thr 16286 35 40 16288 Val Tyr Pro Gly Ala Ser Pro Arg Glu Val Glu Ser Val Ser Arg 16289 50 55 16291 Val Leu Glu Ser Gly Leu Ser Ser Val Lys Asn Leu Lys Asn Ile Tyr 16292 65 70 75 16294 Ser Val Ser Ser Lys Glu Ser Ser Thr Val Ser Leu Glu Phe Tyr His 85 90 16297 Gly Thr Asp Leu Asp Leu Val Leu Asn Glu Ile Arg Asp Ala Leu Glu 100 105 16300 Leu Val Lys Ser Ser Leu Pro Ser Lys Ser Gln Thr Pro Arg Ile Phe 16301 115 120 125 16303 Arg Tyr Asn Leu Lys Asn Ile Pro Val Met Glu Ile Val Ile Asn Ser 16304 130 135 140 16306 Val Arg Pro Val Ser Glu Leu Lys Arg Tyr Ala Asp Glu Ile Ile Lys 16307 145 150 155 16309 Pro Gly Leu Glu Arg Leu Asp Gly Val Ala Ile Val Thr Val Asn Gly 165 170 16312 Gly Ser Lys Lys Arg Val Leu Ile Glu Val Ser Gln Asn Arg Leu Glu 16313 . 180 185 16315 Ser Tyr Gly Leu Ser Leu Ser Arg Ile Ser Ser Ile Ile Ala Ser Gln 16316 195 200 16318 Asn Leu Glu Leu Ser Ala Gly Asn Ile Leu Glu Asn Asn Leu Glu Tyr 16319 210 215 220 16321 Leu Val Glu Val Ser Gly Lys Phe Lys Ser Ile Glu Glu Ile Gly Asn 16322 225 230 235 16324 Val Val Ile Ala Tyr Lys Ile Pro Asp Ile Ser Ser Gly Ile Asn Leu 245 250 16327 Ser Pro Ile Glu Ile Lys Leu Lys Asp Ile Ala Asn Ile Lys Thr Asp 260 265

16330 16331		Glu	Asp 275	Leu	Ser	Glu	Tyr	Val 280	Glu	Tyr	Asn	Gly	Leu 285	Pro	Ser	Ile
16333				Val	Gl'n	Lys	_		Asp	Ser	Asn			Ala	Val	Ser
16334		290					295					300				
16336 16337		Val	Val	Met	Asn	Glu 310	Ile	Glu	Lys	Leu	Lys 315	Leu	Ser	Met	Pro	Lys 320
16339	Asp	Met	Lys	Leu		Ile	Ala	Ser	Asp		Thr	Asp	Phe	Ile	Lys 335	Ala
16340	_		_		325		_	_		330	<b>5</b> 1.	<b>a1</b> .	- 1 -	34 - L		
16342 16343	Ser	iie	Ser	340	vaı	val	Asn	Ser	345	Tyr	Pne	GIŻ	Ala	мет 350	Leu	АТА
16345	Ile	Phe	Val	Ile	Phe	Phe	Phe	Leu	Arg	Ser	Phe	Arq	Ala	Thr	Ile	Ile
16346			355					360	_			_	365			
16348	Ile	Gly	Ile	Ser	Ile	Pro	Ile	Ala	Ile	Val	Leu	Thr	Phe	Cys	Leu	Met
16349		370					375					380				
16351	Tyr	Phe	Val	Asn	Ile	Ser	Leu	Asn	Ile	Met	Ser	Leu	Ala	Gly	Leu	Ala
16352	385					390					395					400
16354	Leu	Gly	Ile	Gly	Met	Val	Val	Asp	Cys	Ser	Ile	Val	Val	Ile	Asp	Asn
16355					405					410					415	
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16358				420					425					430		
16360	Leu	Gly	Ala	Gln	Glu	Met	Met	Leu	Pro	Ile	Thr	Ser	Ser	Thr	Phe	Thr
16361			435					440					445			
16363	Ser	Ile	Cys	Val	Phe	Gly	Pro	Phe	Leu	Ile	Phe	Lys	Ser	Glu	Leu	Gly
16364		450	_				455					460				
16366	Val	Tyr	Gly	Asp	Phe	Phe	Lys	Asp	Phe	Thr	Phe	Thr	Ile	Val	Ile	Ser
16367	465	_		_		470					475					480
16369	Leu	Gly	Val	Ser	Leu	Leu	Val	Ala	Ile	Phe	Leu	Val	Pro	Val	Leu	Ser
16370					485					490					495	
16372	Ser	His	Tyr	Val	Gly	Leu	Tyr	Thr	Ser	Phe	Gln	Lys	Asn	Ile	Lys	Asn
16373				500					505					510		
16375	Ala	Phe	Ile	Arg	Lys	Ile	Asp	Ala	Phe	Phe	Ala	Ser	Ile	Tyr	Tyr	Phe
16376			515					520					525			
16378	Leu	Glu	Phe	Leu	Tyr	Ile	Asn	Leu	Leu	Asn	Ile	Val	Leu	Asn	His	Lys
16379		530			_		535					540				
16381	Leu	Ile	Phe	Gly	Leu	Ile	Val	Phe	Phe	Ser	Phe	Ile	Gly	Ser	Leu	Leu
16382						550					555					560
16384	Leu	Gly	Leu	Leu	Leu	Asp	Val	Thr	Thr	Phe	Thr	Arg	Gly	Lys	Glu	Asn
16385					565					570					575	
16387	Ser	Ile	Thr	Ile	Asn	Leu	Asn	Phe	Pro	His	Lys	Thr	Asn	Leu	Glu	Tyr
16388				580					585					590		
16390	Ala	Lys	Phe	Tyr	Ser	Asn	Arg	Phe	Leu	Glu	Ile	Val	Lys	Ser	Glu	Ala
16391		_	595	_				600					605			
16393	Lys	Gly	Tyr	Lys	Ser	Ile	Ile	Ala	Thr	Leu	Arg	Ala	Asp	Arg	Ile	Thr
16394	_	610	_	_			615					620				
16396	Phe	Asn	Val	Leu	Phe	Pro	Leu	Lys	Glu	Glu	Ser	Arg	Asp	Asn	Leu	Thr
16397						630		_			635	-	-			640
16399	Gln	Ser	Val	Asp	Tyr	Asp	Ser	Ile	Lys	Tyr	Lys	Ile	Met	Asn	Arg	Ile
16400				-	645	•			-	650	-				655	
16402	Gly	Asn	Leu	Tyr	Pro	Glu	Phe	Asn	Ile	Glu	Pro	Ser	Ile	Ser	Gly	Asn

Input Set : N:\COPIES\EBONY\PB481USs1.txt
Output Set: N:\CRF3\05082001\I830230.raw

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665
     16405 Ala Leu Gly Gly Gly Asp Ser Ile Lys Ile Lys Ile Ser Ala Asn Asp
     16406 675
                                  -680
     16408 Phe Glu Tyr Ile Lys Asp Tyr Gly Lys Ile Leu Val Ser Met Leu Lys
     16409 690
                                 695
                                                     700
     16411 Lys Glu Ile Pro Glu Leu Val Asn Pro Arg Leu Ser Ile Ser Asp Phe
     16412 705
                             710
                                                 715
     16414 Gln Leu Gln Ile Gly Val Glu Ile Asp Arg Ala Leu Val Tyr Asn Tyr
                         725
                                             730
     16417 Gly Ile Asp Met Asn Thr Ile Leu Asn Glu Leu Lys Ala Asn Ile Asn
     16418
                     740
                                         745
    16420 Gly Val Val Ala Gly Gln Tyr Val Glu Lys Gly Leu Asn Tyr Asp Ile
    16421 755
                                     760
    16423 Val Leu Lys Leu Asp Arg Met Asp Val Lys Asn Leu Lys Asp Leu Glu
                                775
     16426 Lys Ile Phe Ile Thr Asn Ser Ser Gly Val Lys Ile Pro Phe Ser Ser
                             790
                                                795
    16429 Ile Ala Thr Phe Glu Lys Thr Asn Lys Ala Glu Ser Ile Tyr Arg Glu
                       805
                                            810
                                                                815
    16432 Asn Gln Ala Leu Thr Ile Tyr Leu Asn Ala Gly Ile Ser Pro Asp Asp
                     820
                                         825
    16435 Asn Leu Thr Gln Val Thr Ala Lys Val Val Asp Phe Ile Asn Asn Lys
                  835
                                     840
    16438 Val Pro His Lys Glu Gly Ile Thr Leu Lys Val Glu Gly Glu Tyr Asn
    16439 850
                                 855
                                                     860
    16441 Glu Phe Ser Asn Ile Met Asn Gln Phe Lys İle Ile Ile Met Met Ala
                             870
                                                 875
    16444 Ile Ile Val Val Phe Gly Ile Met Ala Ser Gln Phe Glu Ser Phe Leu
                         885
                                             890
    16447 Lys Pro Phe Ile Ile Ile Phe Thr Ile Pro Leu Thr Ala Ile Gly Val
                     900
                                         905
    16450 Val Leu Ile His Phe Leu Ala Gly Glu Lys Leu Ser Ile Phe Ala Ala
    16451 915
                                     920
                                                        925
    16453 Ile Gly Met Leu Met Leu Val Gly Val Val Asn Thr Gly Ile Val
    16454 930
                                 935
    16456 Leu Val Asp Tyr Thr Gly Leu Leu Ile Lys Arg Gly Phe Gly Leu Arg
    16457 945
                             950
                                                 955
    16459 Glu Ala Ile Ile Glu Ser Cys Arg Ser Arg Leu Arg Pro Ile Leu Met
                        965
                                            970
    16462 Ser Ser Leu Thr Ser Ile Ile Gly Leu Ile Pro Met Ala Phe Ser Ser
                    980
                                         985
    16465 Gly Ser Gly Asn Glu Leu Leu Lys Pro Ile Ala Phe Thr Phe Ile Gly
    16466 995
                                  1000
                                                       1005
    16468 Gly Met Thr Ala Ser Thr Phe Leu Thr Leu Phe Phe Ile Pro Met Leu
    16469 1010
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                    1030
E--> 16472(025)/025
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pp 21-22

Input Set : N:\COPIES\EBONY\PB481USs1.txt
Output Set: N:\CRF3\05082001\I830230.raw

18634 <212> TYPE: PRT 18635 <213> ORGANISM: Homo sapiens 18637 <400> SEQUENCE: 412 18638 Met Lys Lys Ala Asn Phe Leu Ser Thr Asn Phe Leu Ile Leu Leu 18639 1 5 18641 Val Cys Phe Val Asn Val Asn Leu Phe Ser Lys Asp Ile Phe Lys Phe 18642 18644 Lys Leu Val Asp Gln Phe Phe Pro Phe Tyr Tyr Lys Asn Asn Lys Gly 35 18647 Glu Tyr Glu Gly Leu Ile Phe Ser İle Leu Asp Lys Trp Ala Lys Asp 50 55 18650 Asn Asn Ala Asp Ile Met Val Glu His Ile Asp Asn Leu Asn Glu Ser 70 18653 Glu Ile Glu Asp Glu Ala Ile Tyr Leu Gly Leu Thr Tyr Asn Val Lys 85 90 18656 Leu Asn Asp Phe Phe Tyr Phe Lys Ser Glu Leu Ala Arg Ser Ile Ser 110 100 105 18659 Ile Leu Phe Phe Lys Asn Ser Asn Lys Lys Tyr Lys Asn Thr His Ser. 115 120 125 18662 Thr Phe Leu Ser Asn Phe Asn Ile Gly Val Ile Lys Asn Thr Ile Tyr 135 140 18665 Glu Asp Ile Leu Arg Leu Lys Asn Val Asn Thr Ile Phe Leu Ala Asp 18666 145 150 155 18668 Asn Ser Gln Glu Leu Val Leu Ala Leu Lys Asn Asp Lys Val Asp Tyr 170 165 18671 Ile Tyr Gly Asp Cys Lys Thr Leu His Tyr Ile Ala Asn Asn Phe Leu 180 185 18674 Ser Glu Asp Leu Val Ile Phe Thr Gly Asp Val Phe Tyr Ser Ile Lys 195 200 205 18677 Asn Arg Val Ala Ile Ser Arg Asn Ala Pro Glu Ile Val Lys Asn Leu 210 215 220 18680 Asn Leu Asp Leu Phe Ser Tyr Leu Met Lys Met Pro Glu Glu Leu Val 18681 225 230 235 18683 Phe Ser Phe Leu Asp Ser Asn Ala Lys Gly Ser Phe Val Asp Val Gly 245 250 18686 Leu Tyr Asn Asp Tyr Pro Pro Leu Ser Phe Ile Asn Ser Gln Gly Lys 18687 260 265 18689 Leu Ser Gly Ile Leu Val Asp Leu Trp Asn Leu Leu Ser Arg Gln His 280 275 18692 Ile Phe Lys Pro Ile Phe Lys Gly Phe Ser Lys Glu Asp Ile Lys Lys 295 18695 Ser Leu Asp Gly Lys Ser Val Gly Ile Phe Gly Gly Ile Ile Ser Asn 310 315 18698 Asp Ser Val Leu Glu Asn Val Asn Tyr Val Val Ser Lys Pro Ile Tyr 325 330 18701 Pro Leu Asn Phe Lys Phe Tyr Ser Lys Asp Leu Ser Asn Asp Ala Gly 340 345 18704 Pro Ile Asn Ser Gln Phe Ile Asp Phe Asn Phe Asn Asn Ile Gln Leu 355 360

PATENT APPLICATION: US/09/830,230 DATE: 05/08/2001 TIME: 12:00:34

18707			Asn	Lys	Asp	Ile		Asn	Asn	Phe	Ile	Asp 380	Ile	Val	Asn	Asn
18708		370	<b>~1</b>	nh.	T1.	C1	375	Com	т1.	mhm	mh~		m	T 0	Tou	T
18710		туr	GIY	Pne	11e		ASN	ser	116	Thr		гÃг	TYL	Leu	Leu	Lys 400
18711			G1	ш	3	390	3	T	T	C ~ **	395	1 an	Com	Tla	Dho	
18713		Asn	GIĀ	Tyr		GIY	Arg	Leu	гĀг		туг	ASP	ser	TIE		ASI
18714		•		D	405	17 1	<b>.</b>	*1-	T1.	410	3	*	т1.	m	415	37.0.3
18716	_	Asn	Arg		Leu	vaı	Leu	Ala		Asp	ASI	Arg	TTE		гàг	vai
18717		<b>.</b> .		420	•	•		-1-	425	<b>3</b>	3	T1.	C	430	C1	C
18719	•	Lys		шe	Leu	Asn	Ser		Pne	Asp	Asp	ше		Pne	GIU	Ser
18720			435	*1.		<b>.</b>		440	<b>.</b>		<b>T</b>	01	445	T1.		G
18722			GIn	ше	Asp	ьys		Trp	Leu	Asp	гàг		GIU	тте	ASI	ser
18723		450	-1-		<b>a</b>	<b></b>	455	T1.	16- L		<b>.</b>	460	T	Dh.	3	T1.
18725		Arg	ıте	Asn	Ser		гàг	TTE	мет	ASII		vaı	гĀ2	Pne	ASII	
18726		<b>01</b>	T	<b>+1</b> _	m	470	C	T	3	N	475	T 011	7~~	T 0	710	480
18728		GIU	гĀг	шe	485	rea	ser	гуѕ	ASII	490	гЛЯ	Leu	ASII	ьeu	495	vai
18729			m	m		T1 -	<b>3</b>	m	37-1		31.	3	3	M		C1
18731	ьys	ASN	Trp		Pro	ire	ASP	туг	505	GIU	Ala	ASII	ASII	510	ьуѕ	GIÀ
18732 18734	T1-	3	G1	500	T	T	3	T		7 ~~	Wat	nha	Cor		t ou	7~~
		ASII		Pne	Leu	ьeu	ASP	520	TIE	AIG	met	rne	525	GIY	пеп	ALG
18735 18737		7	515	т1 о	T	17.1	111.0		Con	Ton	N an	T 011		Tura	T OU	Tlo
18738	PHE	530	TIE	116	пуъ	Val	535	261	361	ьeu	изр	540	nys	цуз	цец	116
18740	T v/c		Clv	Tuc	Tlo	λan		Lou	λen	Thr	λen		Thr	λen	Sar	Λen
18741	-	ser	GIA	гуу	ire	550	met	ьęи	ASII	1111	555	AIG	T 111	мэр	261	560
18743		λen	λen	Va 1	Dho		Tla	Luc	T.au	Δen		Δτα	Tle	Pro	T.011	
18744	Leu	ASP	ASII	Val	565	ASII	TIE	цуз	цец	570	261	пту	116	FIO	575	IYI
18746	Tla	Dha	Ser	Δen		Lve	Δra	Val	T.e.ii		Ser	Δrσ	Ser	Len		T.vs
18747	110	1 110	001	580	<b>1</b> ,5	<b>1</b> ,5	**** 9	, u _	585	110	001	9	001	590	010	2,2
18749	Phe	Δla	Tle		Asp	Phe	Len	Tur		Lvs	Asn	Leu	Ala		Asn	Tle
18750	1		595	200			Lou	600	001				605	001		
18752	Lvs	Ser		Len	Tle	Len	Val		Ser	Phe	Asn	Glu		Leu	Leu	Leu
18753	<b>-</b> 1, 5	610	2,5	LCu		200	615	001	001			620				200
18755	Leu		Lvs	Glv	Lvs	Va 1		Glv	Tle	Tle	Ser		Glu	Tvr	Thr	Ala
18756		-1-		<b>0</b> -1	-,-	630		U-1			635			-1-		640
18758	-	λla	Val	Phe	Glu		Leu	Asn	Ile	Asp		Val	Glu	Lvs	Ile	
18759					645					650				-1-	655	
18761	Thr	Phe	Ara	Asp		Ala	Phe	Asp	Leu		Leu	Ala	Ile	Tvr	Asn	Gln
18762			5	660					665					670		
18764	Asp	Tvr	Ile		Lvs	Glu	Ile	Ile		Lvs	Val	Val	Met	Ara	Ser	Asn
18765	E	-1-	675		-1-			680		-1-			685	5		
18767	Val	Asp	Ser	Gln	Met	Tvr	Leu	Asn	Asp	Trp	Lvs	Phe	Asp	Ile	Tyr	Tyr
18768		690				-1-	695					700	•			-
18770	Lys		Arq	Ser	Ile	Arg		Lys	Asn	Phe	Lys		Leu	Val	Ile	Thr
18771			,			710		•			715					720
18773		Ile	Ile	Phe	Tyr	Phe	Thr	Phe	Leu	Gly	Phe	Val	Ile	Ile	Phe	Met
18774					725					730					735	
18776	Phe	Arg	Leu	Ser	Phe	Glu	Gln	Lys	Arg	Arg	Tyr	Ser	Phe	Val	Met	Asn
18777		-	-	740				-	745	-	-			750		
18779	Glu	Lys	Lys	Ile	Ala	Glu	Ala	Ala	Asn	Ala	Ala	Lys	Thr	Ile	Phe	Ile

Input Set : N:\COPIES\EBONY\PB481USsl.txt
Output Set: N:\CRF3\05082001\I830230.raw

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18783		770				•	775	_				780	-			
18785	Ala	Thr	Glu	Leu	Leu	Asp	Thr	Thr	Ile	Leu	Thr	Asp	Val	Gln	Lys	Asp
18786						790					795					800
18788	Tyr	Val	Arg	Met	Ile	Asn	Tyr	Ser	Ser	Asp	Ser	Leu	Leu	Ser	Leu	Ile
18789					805					810					815	
18791	Asp	Asp	Ile	Leu	Tyr	Leu	Ser	Lys	Ile	Asp	Val	Asn	Glu	Leu	Tyr	Val
18792				820					825					830		
18794	Glu	Ser	Gln	Glu	Ile	Asp	Leu	Glu	Ser	Glu	Met	Glu	Met	Val	Leu	Lys
18795			835					840					845			
18797	Ala	Phe	Gln	Ser	Gln	Cys	Ala	Lys	Lys	Asn	Ile	Asp	Leu	Phe	Ser	Tyr
18798		850					855					860				
18800	Ser	Lys	Ser	Ile	Phe		Asn	Tyr	Ile	Lys		Asp	Ile	Val	Lys	Ile
18801						870					875					880
18803	Lys	Gln	Val	Leu	Ile	Asn	Leu	Ile	Gly	Asn	Ala	Phe	Lys	Phe	Thr	Asp
18804					885					890					895	
18806	Asp	Gly	Val		Val	Leu	Asn	Tyr		Glu	Val	Cys	Arg		Arg	Thr
18807				900			_	_	905			_		910		
18809	_	Gly		Arg	Val	Leu	Val		Val	Glu	Phe	Lys		Ile	Asp	Thr
18810		_	915			_	~ .	920	_,	_	_		925		_,	1
18812	_	-	GLY	He	Glu	Lys		Asn	Phe	Ser	rys		Phe	Glu	тте	Phe
18813		930	-1			<b>~</b>	935	<b>a</b>		** 1		940	<b>01</b>		<b>01</b>	T
18815	_	GIn	GIU	Asp	Asp		Ser	Ser	Arg	vaı		GIU	GIĀ	Ala	GTÅ	
18816		T	C	T1.	C	950	C1	T	T1-	3 m	955	Wat	C1	c1	T 0.1	960
18818	GIY	ьeu	ser	TTE	965	Arg	GIU	ьeu	тте	970	Leu	мес	GIA	GTA	975	GIY
18819 18821	т1.	7 l a	Val	700			Val	C1++	C1		mhr	Thr	Dho	Sor		Mot
18822	116	ніа	Val	980	ser	гуу	Val	Gry	985	GIY	1111	1111	FIIE	990	rne	Met
18824	T.Au	Pro	Dha		T.e.11	Glv	Ser	Glu		T.vc	Ser	T.vs	Lvs		Ser	Tle
18825	пеа	110	995	БСи	пси	OLY		1000	пси	<b>1</b>	OCI		1005	шеи	DCI	110
18827	Asn	Ara		Gln	Ser	Va 1			Asp	Asn	Lvs			Asn	Val	Leu
18828		1010					L015	1				L020				
18830			Gln	Lys	Ser			Ile	Phe	Glu			Ser	Ile	Leu	Leu
18831		_		-		.030	•				035	-				040
18833			Ser	Ser	Asn	Val	Arg	Tyr	Val	Ala	Ser	Phe	Glu	Asp	Ala	Tyr
18834		-			.045		•	_		1050					.055	_
18836	Lys	Val	Phe	Lys	Lys	Tyr	Pro	Ser	Tyr	Asn	Phe	Val	Tyr	Ile.	Asn	Val
18837				.060					1065					1070		
18839	Asn	Asn	Asp	Asn	Ile	Gln	Glu	Gly	Ile	Arg	Leu	Ala	Asn	Asn	Ile	Glu
18840		1	1075				1	.080				1	1085			
18842	Arg	Leu	Asn	Ser	Asp	Val	Gln	Ile	Ile	Phe	Leu	Phe	Tyr	Tyr	Leu	Asp
18843		L090					.095					100				
18845		Lys	Ala	Leu			Leu	Lys	Tyr			Val	Lys	Lys		
18846		)				110					.115					120
18848	Met	Gly	Leu			Cys	Ser	Ile			Lys	Lys	Glu			Pro
18,849	_				.125			_	_	.130		_			135	
18851	Glu	Met			Glu	Asp	Leu			Ile	Asp	Ser			Arg	Ile
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E-->

E-->

Input Set : N:\COPIES\EBONY\PB481USsl.txt
Output Set: N:\CRF3\05082001\I830230.raw

18854 Lys Glu Pro Ile Asn Val Leu Ile Ala Glu Asp Asn Gln Val Asn Gln 1165 1160 18855 1155 18857 Lys Val Leu Lys Asp Ile Leu Val Val Ile Gly Ile Asn Glu Asn Phe 18858 1170 1175 1180 18860 Ile Asp Val Val Asp Asp Gly Val Lys Ala Leu Lys Ser Leu Lys Asp E--> 1886( 185 ) 1190 1195 18863 Lys Lys Tyr Thr Ile Ser Phe Ile Asp Ile Arg Met Pro Arg Tyr Asp 1205 1210 1215 18866 Gly Phe Ser Val Ala Lys Glu Ile Arg Lys Phe Glu Lys Ala Lys Asn 18867 1220 1225 18869 Leu Lys Pro Cys Val Leu Val Ala Val Thr Ala His Ala Leu Gln Glu 18870 1235 1240 1245 18872 Tyr Lys Asp Lys Cys Leu Ala Ser Gly Met Asn Asp Tyr Ile Ser Lys 18873 1250 1255 1260 18875 Pro the His Ile Ser Ser Ile Lys Thr Ile Leu Lys Lys Tyr Leu Gln 1275 1280 E--> 18876 265 ) 1270 18878 Phe Glu Val Asp Asp Ile Gly Glu Asn Glu Asn Leu Asn Gln Leu Val **18879 1285 1290 1295** 18881 Lys Phe Pro Asn Leu Asp Val Asn Arg Ala Leu Lys Glu Leu Asn Leu 18882 1300 1305 1310 18884 Ser Tyr Val Ser Tyr Ser Glu Leu Cys Arg Gly Leu Val Asp Phe Ile 18885 1315 1320 1325 18887 Ser Ile Asn Ile Ile Asp Leu Glu Lys Ala Phe Asp Glu Glu Asp Leu 18888 1330 1335 1340 18890 Ser Leu Ile Lys Asp Ile Ser His Ser Ile Ser Gly Ala Leu Ser Asn E--> 1889( 345 ) 1350 1355 18893 Met Arg Ser Glu Leu Tyr Lys Asp Phe Gln Lys Ile Glu Thr Ser Lys 18894 . 1365 1370 18896 Asp Ser Ile Ser Glu Leu Lys Lys Met Tyr Ser Phe Val Lys Asp Asp 18897 1380 1385 18899 Leu Phe Gln Leu Ile Ser Asp Ile Lys Glu Asn Ile Leu Phe Glu Ser 18900 1395 1400 1405 18902 Glu Ile Val Ser Glu Asn Lys Leu Tyr Phe Lys Asn Asn Asp Gln Phe 18903 1410 1415 1420 18905 Leu Asn Leu Leu Asn Lys Leu Leu Ile Gly Ile Lys Thr Arg Lys Pro
1890 425 1430 1435 1440 18908 Arg Glu Tyr Lys Glu Ile Leu Glu Ser Ile Asn Lys Tyr Val Leu Asp 18909 1445 1450 18911 Asp Asn Ile Gln Val Leu Phe Ser Asp Leu Arg Arg Asn Leu Arg Leu 18912 1460 1465 1470 18914 Tyr Arg Phe Ala Glu Ser Ser Lys Ile Leu Glu Glu Ile Ile Glu Met 18915 1475 1480 18917 Leu Asn Asn Lys Arg Tyr 18918 1490 18920 <210> SEQ ID NO: 413 18921 <211> LENGTH: 1477 pg 24-25 18922 <212> TYPE: PRT 18923 <213> ORGANISM: Homo sapiens 18925 <400> SEQUENCE: 413



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18930 18932	Tyr	Glu	Gly	20 Leu		Phe	Ser	Ile	25 Leu	Asp	Lys	Trp	Ala	30 Lys	Asp	Asn
18933			35	<b>~</b> 1			-1	40	-,	_	_	_	45	<b>01</b>	~	0.1
18935 18936		50					55					60				
18938 18939	Ile 65	Glu	Asp	Glu	Ala	Ile 70	Tyr	Leu	Gly	Leu	Thr 75	Tyr	Asn	Val	Lys	Leu 80
18941 18942	Asn	Asp	Phe	Phe	Tyr 85	Phe	Lys	Ser	Glu	Leu 90	Ala	Arg	Ser	Ile	Ser 95	Ile
18944	Leu	Phe	Phe	Lvs		Ser	Asn	Lvs	Lvs		Lvs	Asn	Thr	His		Thr
18945				100					105					110		
18947 18948	Phe	Leu	Ser 115	Asn	Phe		IIe	GLy 120	Val	IIe	Lys	Asn	Thr 125	IIe	Tyr	Glu
18950	Asp	Ile		Arq	Leu	Lys	Asn		Asn	Thr	Ile	Phe	Leu	Ala	Asp	Asn
18951	-	130				•	135					140			•	
18953	Ser	Gln	Glu	Leu	Val	Leu	Ala	Leu	Lys	Asn	Asp	Lys	Val	Asp	Tyr	Ile
18954						150					155					160
18956	Tyr	Gly	Asp	Cys		Thr	Leu	His	$\mathtt{Tyr}$		Ala	Asn	Asn	Phe		Ser
18957	- 1	_	_		165	1	<b></b> 1	~ 1	_	170	_,	-	_	- 1	175	_
18959 18960	GIu	Asp	Leu	180	iie	Phe	Thr	GIĀ	185	vaı	Pne	Tyr	Ser	11e	ьуs	Asn
18962	λra	Va l	λla		Sor	λνα	λen	λla		Clu	Tla	Val	Luc		Lau	λen
18963	nr 9	Val	195	116	361	Arg	ASII	200	110	GIU	116	vai	205	ASII	Deu	ASII
18965	Leu	Asp		Phe	Ser	Tvr	Leu		Lvs	Met	Pro	Glu		Leu	Val	Phe
18966		210				-1-	215		-1-			220				
18968	Ser	Phe	Leu	Asp	Ser	Asn	Ala	Lys	Gly	Ser	Phe	Val	Asp	Val	Gly	Leu
18969						230					235					240
18971	Tyr	Asn	Asp	Tyr		Pro	Leu	Ser	Phe		Asn	Ser	Gln	Gly		Leu
18972	_				245					250					255	
18974		Gly	Ile		Val	Asp	Leu	Trp		Leu	Leu	Ser	Arg		His	Ile
18975 <sup>.</sup> 18977		T	Dwo	260	Dho	T	C1	Dho	265	T	C1	7.00	т1-	270	T	Cor
18978	Pile	rÃ2	275	116	Pile	гуѕ	СГА	280	ser	гу	GIU	ASP	285	пÃР	пÃ2	ser
18980	Len	Asn		T.vs	Ser	Va 1	G1 v		Phe	Glv	Glv	TIE		Ser	Asn	Asn
18981		290	011	<i>D</i> <sub>1</sub> <i>D</i>	001	,	295			017		300		001		1101
18983	Ser		Leu	Glu	Asn	Val		Tyr	Val	Val	Ser		Pro	Ile	Tyr	Pro
18984						310		-			315	-			-	320
18986	Leu	Asn	Phe	Lys	Phe	Tyr	Ser	Lys	Asp	Leu	Ser	Asn	Asp	Ala	Gly	Pro
18987					325					330					335	
18989	Ile	Asn	Ser		Phe	Ile	Asp	Phe		Phe	Asn	Asn	Ile		Leu	Asn
18990	T	n	T	340	т1 -	17- 1	<b>3</b>	<b>.</b>	345	T1 -	3	<b>+1</b> -	37- 3	350	3	C
18992 18993	гÃ2	ASN	Lуs 355	ASP	тте	val	ASN	Asn 360	Lue	тте	ASP	11e	765	ASN	ASD	ser
18995	Tvr	Glv		Tlo	Glu	Δen	Ser		ጥኮድ	Thr	Lve	ጥሆኖ		Lein	T.vc	Leu
18996	-1-	370	1116	TTE	3±u	4911	375	116	T 11T	7 114	₽¥ 2	380	ьcu	ш÷п	בעם	_cu
18998	Asn		Tyr	Asn	Glv	Ara		Lys	Ser	Tyr	Asp		Ile	Phe	Asn	Lys
			• -		- 4	,	-	•		• -						

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,230

DATE: 05/08/2001
TIME: 12:00:34

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19005				420					425					430		
19007	Leu	Gln	Ile	Asp	Lys	Asn	Trp	Leu	Asp	Lys	Glu	Glu	Ile	Asn	Ser	Ser
19008			435					440					445			
19010	Arg	Ile	Asn	Ser	Tyr	Lys	Ile	Met	Asn	Lys	Val	Lys	Phe	Asn	Ile	Glu
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19016	Asn	Trp	Tyr	Pro	Ile	Asp	Tyr	Val	Glu	Ala	Asn	Asn	Tyr	Lys	Gly	Ile
19017					485					490					495	
19019	Asn	Gln	Phe	Leu	Leu	Asp	Lys	Ile	Arg	Met	Phe	Ser	Gly	Leu	Arg	Phe
19020				500		_	-		505					510		
19022	Asn	Ile	Ile	Lys	Val	His	Ser	Ser	Leu	Asp	Leu	Lys	Lys	Leu	Ile	Lys
19023			515	-				520		_		-	525			_
19025	Ser	Gly	Lys	Ile	Asp	Met	Leu	Asn	Thr	Asn	Ala	Thr	Asp	Ser	Asn	Leu
19026		530	•		-		535					540	_			
19028	Asp	Asn	Val	Phe	Asn	Ile	Lys	Leu	Asn	Ser	Arg	Ile	Pro	Leu	Tyr	Ile
19029	_				•	550	-				555				-	560
19031	Phe	Ser	Asn	Lys	Lys	Arg	Val	Leu	Pro	Ser	Arg	Ser	Leu	Glu	Lys	Phe
19032				•	565					570	-				575	
19034	Ala	Ile	Leu	Asp	Phe	Leu	Tyr	Ser	Lys	Asn	Leu	Ala	Ser	Asn	Ile	Lys
19035				580			-		585					590		-
19037	Ser	Lys	Leu	Ile	Leu	Val	Ser	Ser	Phe	Asn	Glu	Ala	Leu	Leu	Leu	Leu
19038		-	595					600					605			
19040	Tyr	Lys	Gly	Lys	Val	Asp	Gly	Ile	Ile	Ser	Asp	Glu	Tyr	Thr	Ala	Ala
19041	-	610	-	-		-	615				-	620	_			
19043	Ala	Val	Phe	Glu	Glu	Leu	Asn	Ile	Asp	Asp	Val	Glu	Lys	Ile	Pro	Thr
19044						630			-	•	635		_			640
19046	Phe	Arg	Asp	Leu	Ala	Phe	Asp	Leu	Ser	Leu	Ala	Ile	Tyr	Asn	Gln	Asp
19047		•	•		645		-			650			-		655	-
19049	Tyr	Ile	Leu	Lys	Glu	Ile	Ile	Gln	Lys	Val	Val	Met	Arg	Ser	Asn	Val
19050	•			660					665				-	670		
19052	Asp	Ser	Gln	Met	Tyr	Leu	Asn	Asp	Trp	Lys	Phe	Asp	Ile	Tyr	Tyr	Lys
19053	-		675		_			680	_	-		_	685	_	_	_
19055	Ser	Arg	Ser	Ile	Arg	Phe	Lys	Asn	Phe	Lys	Phe	Leu	Val	Ile	Thr	Phe
19056		690			_		695			•		700				
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19059				•		710			_		715					720
19061	Arq	Leu	Ser	Phe	Glu	Gln	Lys	Arq	Arg	Tyr	Ser	Phe	Val	Met	Asn	Glu
19062	-				725		•	_	-	730					735	
19064	Lys	Lys	Ile	Ala	Glu	Ala	Ala	Asn	Ala	Ala	Lys	Thr	Ile	Phe	Ile	Ala
19065	-	-		740					745		-			750		
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19068			755		•		-	760				-	765			
19070	Thr	Glu	Leu	Leu	Asp	Thr	Thr		Leu	Thr	Asp	Val	Gln	Lys	Asp	Tyr
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	19074 19076		Ile	Leu	Tyr	Leu	790 Ser	Lys	Ile	Asp	Val	795 Asn	Glu	Leu	Tyr	Val	800 Glu
	19077	<b>.</b>	<b>01</b> .	<b>a</b> 1	<b>~1</b> -	805	•	<b>01</b>	<b>a</b>	<b>01</b>	810	<b>61</b>		17-1	<b>.</b>	815	<b>31</b> -
	19079 19080	ser	GIN	GIU	820	ASP	Leu	GIU	ser	825	мес	GIU	met	Val	830	ràs	Ala
	19082 19083	Phe	Gln	Ser 835	Gln	Cys	Ala	_	Lys 840		Ile	Asp	Leu	Phe 845	Ser	Tyr	Ser
	19085	Lys	Ser		Phe	Asn	Asn				Gly	Asp	Ile		Lys	Ile	Lys
	19086		850					855					860				
	19088		Val	Leu	Ile	Asn		Ile	Gly	Asn	Ala		Lys	Phe	Thr	Asp	
	19089 19091		Va 1	Tla	17 a 1	Lau	870	ጥኒኒዮ	Glu	Glu	Val	875 Cvs	λνα	Thr	Δrσ	Thr	880 Asp
	19092					885					890	•				895	
	19094	Gly	Asn	Arg		Leu	Val	Thr	Vaļ		Phe	Lys	Val	Ile		Thr	Gly
	19095		0.1	- 1	900		<b>a</b> 1	•	<b>D</b> 1	905	•	T1.	<b>D</b> 1	<b>01</b>	910	nl	•
	19097 19098	Lys	GIY	915	GIU	гàг	GIU	Asn	920	Ser	ьуs	тте	Pne	925	ше	Pne	ьуs
	19100	Gln	Glu		Asp	Ser	Ser	Ser		Val	His	Glu	Gly		Gly	Leu	Gly
	19101		930	•				935	-				940		_		-
	19103		Ser	Ile	Ser	Arg		Leu	Ile	Arg	Leu		Gly	Gly	Leu	Gly	
	19104		**. 1	•		<b>.</b>	950	<b>a1</b>	<b>01</b>	<b>01</b>	m 1	955	D1		Dh.	16- L	960
	19106 19107	Ala	vaı	Asp	Ser	ьуs 965	vaı	GLY	GIU	GIĀ	970	Thr	Pne	ser	Pne	мет 975	Leu
	19109	Pro	Phe	Leu	Leu		Ser	Glu	Leu	Lys		Lys	Lys	Leu	Ser		Asn
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	19112 19113	Arg	Phe	Gln 995	Ser	Val	Asn		Asp 1000	Asn	Lys	Val		Asn 1005	Val	Leu	Leu
	19115	Ser	Gln		Ser	Ile	Lys			Glu	His	Cys			Leu	Leu	Gly
	19116	1	1010	_			1	015				_ 1	.020				_
	19118		Ser	Ser	Asn			Tyr	Val	Ala			Glu	Asp	Ala		
E>	1 <b>9110</b> 19121			T	T *** 0		.030	Con	M···	200		.035	M	T10	) an		040
	19121	vaı	Pile	гуу	_	.045	PIQ	ser	ıyı		.050	vai	IYL	116		.055	ASII
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	19127	Leu			Asp	Val	Gln			Phe	Leu	Phe			Leu	Asp	Asn
	19128 19130	Tvc		1075	T vz c	λαn	Tou		.080	Clu	Фих	Val	_	.085	Dro	LOU	Mot
	19131		.090	Leu	гуз	ASII		.095	TÄT	GIY	TYL		100	пåр	PIU	Leu	Mec
	19133			Gly	Ile	Cys			Leu	Tyr	Lys			Phe	Asn	Pro	Glu
E>	1913		)				110					115					120
	19136 19137	Met	Asp	Phe		Asp 125	Leu	Val	Pro		Asp 130	Ser	Ala	Leu		Ile 135	Lys
	19137	Glu	Pro	Tle			Len	Tle	Δla			Asn	Gln	Va 1			Lvs
	19140				140					145					150		-1-
	19142	Val	Leu	Lys	Asp	Ile	Leu	Val	Val	Ile	Gly	Ile	Asn	Glu	Asn	Phe	Ile
	19143	_	_	.155	_	_			160		_	_		165	_	_	_
	19145	Asp	Val	Val	Asp	Asp	Gly	Val	Lys	Ala	Leu	Lys	Ser	Leu	Lys	Asp	Lys

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28275 <221> NAME/KEY: SITE
28276 <222> LOCATION: (416)
28277 <223> OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
28279 <400> SEQUENCE: 630
28280 Ala Gly Asn Thr Val Lys Thr Ala Glu Gly Ala Ser Ser Gly Thr Asp
28281 1
                        -5
28283 Ala Ile Gly Glu Val Val Asp Asn Asp Ala Lys Val Ala Asp Lys Ala
28284
                   20
                                       25
28286 Ser Val Thr Gly Ile Ala Lys Gly Ile Lys Glu Ile Val Glu Ala Ala
28287
28289 Arg Gly Ser Glu Lys Leu Lys Val Ala Ala Ala Lys Glu Gly Asn Glu
          50
                               55
28292 Lys Ala Gly Lys Leu Phe Gly Lys Ala Gly Ala Asn Ala His Gly Asp
28293 65
                                               75
                           70
28295 Ser Glu Ala Ala Ser Lys Ala Ala Gly Ala Val Ser Ala Val Ser Gly
                                           90
28298 Glu Gln Ile Leu Ser Ala Ile Val Lys Ala Ala Asp Ala Ala Glu Gln
28299
                  100
                                      105
28301 Asp Gly Lys Lys Pro Ala Asp Ala Thr Asn Pro Ile Ala Ala Ala Ile
             115
                                  120
                                                      125
28304 Gly Asn Lys Asp Glu Asp Ala Asp Phe Gly Asp Gly Met Lys Lys Asp
         130
                              135
28307 Asp Gln Ile Ala Ala Ile Ala Leu Arg Gly Met Ala Lys Asp Gly
28308 145
                          150
                                              155
28310 Lys Phe Ala Val Lys Asn Asp Glu Lys Gly Lys Ala Glu Gly Ala Ile
                      165
                                          170
28313 Lys Gly Ala Ala Ala Ile Gly Glu Val Val Asp Asn Ala Gly Ala Ala
                 180
                                      185
28316 Lys Ala Ala Asp Lys Asp Ser Val Lys Gly Ile Ala Lys Gly Ile Lys
             195
                                  200
28319 Glu Ile Val Glu Ala Ala Gly Gly Ser Glu Lys Leu Lys Ala Ala Ala
                              215
                                                  220
28322 Ala Glu Gly Glu Asn Asn Lys Lys Ala Gly Lys Leu Phe Gly Lys Val
28323 225
                                              235
```

	28325	Asp	Gly	Ala	Ala	Gly	Asp	Ser	Glu	Ala	Ala	Ser	Lys	Ala	Ala	Gly	Ala
	28326					245					250					255	
	28328	Val	Ser	Ala			Gly	Glu	Gln			Ser	Ala			Lys	Ala
	28329				260					265					270		
	28331	Ala	Gly			Glu	Gln	Asp		Glu	Lys	Pro	Glu		Ala	Lys	Asn
	28332			275					280					285			
	28334	Pro		Ala	Ala	Ala	Ile	_	Lys	Gly	Asn	Gly		Gly	Ala	Glu	Phe
	28335		290					295					300				
	28337		Gln	Asp	Glu	Met		Lys	Asp	Asp	Gln		Ala	Ala	Ala	Ile	
	28338						310					315		_		_	320
	28340	Leu	Arg	Gly	Met		Lys	Asp	Gly	Lys		Ala	Val	Lys	GLY		Asn
	28341		_		_	325	_,				330	-1		_	- 1	335	_
	28343	Glu	Lys	GLu		Ala	Glu	GLY	Ala		Lys	GLu	vaı	Ser		Leu	Leu
	28344		<b>7</b>		340	m 1	. 1 -	**- 1	<b>T -</b>	345	.1-	a1	a1		350	C	G1
	28346	Asp	гаг		vaı	Thr	Ата	vai			Ala		GTÅ		ser	ser	GIA
AK.	28347	m1	3	355	T1 -	<b>a</b> 1	C1	17- 1	360		3	, V	71.	365	V	71-	7
606	28349 28350	THE	370	Ата	ше	стх	GIU	375	Val	ASP	ASII	Add	380	гаг	лаа	MIG	Asp
	28352	Luc		Sor	Val	Thr	Glv.		λla	Luc	Glv	τÌΔ		Glu	Tla	Va l	Glu
٠.	28353		ліа	361	Val	1111	390	116	пта	цуз	GLY	395	цуз	GIU	116	vai	400
16/16/	28355		Δla	Yaa	G1 v	Sar		T.vc	T.e.ii	T.ve	Va1		Δla	Δla	Yaa	Yaa	
-Olo	28356	nru	niu	Auu	GLJ	405	GIU	цу	LCu	цу	410	niu	*****	21.1.4	Auu	415	nuu
	28358	Asn	Asn	Lvs	Glu		Glv	Lvs	Leu	Phe		Lvs	Ala	Glv	Ala		Ala
	28359			-10	420		U-1	-10		425	0-1	-1-		1	430		
	28361	Asn	Glv	Asp		Glu	Ala	Ala	Ser		Ala	Ala	Glv	Ala		Ser	Ala
	28362			435					440				4	445			
	28364	Val	Ser	Gly	Glu	Gln	Ile	Leu	Ser	Ala	Ile	Val	Lys	Ala	Ala	Ala	Ala
	28365		450	-				455					460				
	28367	Gly	Ala	Ala	Asp	Gln	Asp	Gly	Glu	Lys	Pro	Gly	Asp	Ala	Lys	Asn	Pro
	28368	465					470					475					480
	28370	Ile	Ala	Ala	Ala	Ile	Gly	Lys	Gly	Asn	Ala	Asp	Asp	Gly	Ala	Asp	Phe
	28371					485					490					495	
	28373	Gly	Asp	Gly		Lys	Lys	Asp	Asp		Ile	Ala	Ala	Ala		Ala	Leu
	28374				500					505					510		
	28376	Arg	Gly		Ala	Lys	Asp	Gly		Phe	Ala	Val	Lys		Asp	Glu	Lys
	28377	~ 1	_	515					520			_		525	_	_	_
	28379	GIĀ		Ala	GIu	GTĀ	Ala		Lys	Gly	Ala	Ser		Leu	Leu	Asp	гàг
	28380	<b>.</b>	530	<b>.</b>		17- 1	T	535	. 1 -		<b>61</b>	21-	540	<b>a</b>	C1	mh m	11-
	28382		vaı	гÃг	Ala	vaı	_	Tnr	Ala	GIU	GIĀ		ser	ser	GŢĀ	Thr	
	28383		т1.	C1	C1	17 n 1	550	N a n	N a n	A 1 a	<b>3.1</b> a	555	<b>7.1.</b>	λl ¬	N c n	Tuc	560
	28385 28386	Ата	116	GIY.	GIU	565	vai	ASP	ASII	нта	570	гуу	нта	нта	Asp	575	KSP
	28388	Sar	Va 1	Thr	Clv		Δla	T.v.c	G1v	Tla		Glu	Tla	Va l	Glu		Δla
	28389	Der	* a I	TIII	580	116	чта	ב עם	GIY	585	ay 3	Gra	116	7 U.I	590		
	28391	Glv	Glv	Ser		Lvs	Leu	Lvs	Va 1		Ala	Ala	Lvs	Gl v		Asn	Asn
	28392	J-1	J-1	595	JIU	د ړ ــ	cu	~, 5	600				-13	605	J_4		
	28394	Lvs	Glv		Glv	Lvs	Leu	Phe		Lvs	Ala	Glv	Ala		Ala	His	Glv
	28395	-, -	610		1	-1-		615	1	-10		1	620				1
	28397	Asp		Glu	Ala	Ala	Ser		Ala	Ala	Gly	Ala		Ser	Ala	Val	Ser
		•						•			-						

20200						630					635					640
28398		- 1	<b>a</b> 1	T1 -	<b>.</b>	630		<b>-1</b> -	17- 1	T			<b>61</b>	<b>61</b>		
28400	GIŞ	GIU	GIN	ше		ser	Ald	шe	val		Ald	Ald	стй	GIU		Ala
28401	- 1			<b>a</b> 1	645	<b>.</b>	T	n	<b>a</b> 1	650	31.	<b>7</b>		D	655	31-
28403	GLY	Asp	GIn		GTĀ	Lys	ьys	Pro		GLu	АТа	ràs	Asn		ше	Ата
28404				660		_	_		665			_,	_	670	_	~ 3
28406	Ala	Ala		GLy	Asp	Lys	Asp	_	Asp	Ala	Glu	Phe		GIn	Asp	GLY
28407			675					680	_		_	_	685	_		
28409	Met		Lys	Asp	Asp	Gln		Ala	Ala	Ala	Ile		Leu	Arg	Gly	Met
28410		690					695					700				
28412		Lys	Asp	Gly	Lys		Ala	Val	Lys	Asp		Gly	Glu	Lys	Glu	
28413						710					715					720
28415	Ala	Glu	Gly	Ala		Lys	Gly	Val	Ser		Leu	Leu	Asp	Lys		Val
28416					725					730					735	
28418	Lys	Ala	Val	Lys	Thr	Ala	Glu	Gly	Ala	Ser	Ser	Gly	Thr	Ala	Ala	Ile
28419				740					745					750		
28421	Gly	Glu	Val	Val	Ala	Asp	Ala	Ala	Lys	Val	Ala	Asp	Lys	Ala	Ser	Val
28422			755					760					765			
28424	Thr	Gly	Ile	Ala	Lys	Gly	Ile	Lys	Glu	Ile	Val	Glu	Ala	Ala	Gly	Asp
28425		770					775					780				
28427	Ser	Glu	Ala	Ala	Ser	Lys	Ala	Ala	Gly	Ala	Val	Ser	Ala	Val	Ser	Gly
28428	785					790					795					800
28430	Glu	Gln	Ile	Leu	Ser	Ala	Ile	Val	Lys	Ala	Ala	Ala	Ala	Gly	Ala	Ala
28431					805					810			,		815	
28433	Glu	Gln	Asp	Gly	Glu	Lys	Pro	Ala	Glu	Ala	Lys	Asn	Pro	Ile	Ala	Ala
28434				820					825					830		
28436	Ala	Ile	Gly	Lys	Gly	Asp	Gly	Asp	Ala	Asp	Phe	Gly	Glu	Asp	Gly	Met
28437			835					840					845			
28439	Lys	Lys	Asp	Asp	Gln	Ile	Ala	Ala	Ala	Ile	Ala	Leu	Arg	Gly	Met	Ala
28440		850					855					860				
28442	Lys	Asp	Gly	Lys	Phe	Ala	Val	Lys	Asn	Asp	Glu	Lys	Gly	Lys	Ala	Glu
28443	865					870					875					880
28445	Gly	Ala	Ile	Lys	Gly	Ala	Ala	Ala	Ile	Gly	Glu	Val	Val	Asp	Asn	Ala
28446					885					890					895	
28448	Gly	Ala	Ala	Lys	Ala	Ala	Asp	Lys	Asp	Ser	Val	Lys	Gly	Ile	Ala	Lys
28449				900					905					910		
28451	Gly	Ile	Lys	Glu	Ile	Val	Glu	Ala	Ala	Gly	Gly	Ser	Glu	Lys	Leu	Lys
28452			915					920					925			
28454	Ala	Ala	Ala	Ala	Glu	Gly	Glu	Asn	Asn	Lys	Lys	Ala	Gly	Lys	Leu	Phe
28455		930					935					940				
28457	Gly	Lys	Val	Asp	Gly	Ala	Ala	Gly	Asp	Ser	Glu	Ala	Ala	Ser	Lys	Ala
28458						950					955					960
28460	Ala	Gly	Ala	Val	Ser	Ala	Val	Ser	Gly	Glu	Gln	Ile	Leu	Ser	Ala	Ile
28461					965					970					975	
28463	Val	Lys	Ala	Ala	Asp	Ala	Ala	Glu	Gln	Asp	Gly	Lys	Lys	Pro	Ala	Asp
28464				980					985					990		
28466	Ala	Thr	Asn	Pro	Ile	Ala	Ala	Ala	Ile	Gly	Asn	Lys	Asp	Glu	Asp	Ala
28467			995				1	.000				1	.005			
28469	Asp	Phe	Gly	Asp	Gly	Met	Lys	Lys	Asp	Asp	Gln	Ile	Ala	Ala	Ala	Ile
28470	1	010				1	015				1	.020				

Input Set : N:\COPIES\EBONY\PB481USs1.txt
Output Set: N:\CRF3\05082001\I830230.raw

28472 Ala Leu Arg Gly Met Ala Lys Asp Gly Lys Phe Ala Val Lys Gly Asn E--> 28473 025 ) 1030 1035 28475 Asn Glu Lys Gly Lys Ala Glu Gly Ala Ser Ser Gly Thr Asp Ala Ile 1045 1050 28478 Gly Glu Val Val Asp Asn Asp Ala Lys Ala Ala Asp Lys Ala Ser Val 1060 1065 1070 28481 Thr Gly Ile Ala Lys Gly Ile Lys Glu Ile Val Glu Ala Ala Gly Gly 28482 1075 1080 1085 28484 Ser Glu Lys Leu Lys Ala Val Ala Ala Ala Thr Arg Glu Asn Asn Lys pumbering 28485 1090 1095 1100 28487 Growla Gly Lys Leu Phe Gly Lys Val Asp Asp Ala His Ala Gly Asp 1110 E--> 28486 105 1115 28490 Ser Glu Ala Ala Ser Lys Ala Ala Gly Ala Val Ser Ala Val Ser Gly 1135 28491 1125 1130 28493 Glu Gln Ile Leu Ser Ala Ile Val Thr Ala Ala Ala Gly Glu Gln 1145 28494 1140 1150 28496 Asp Gly Glu Lys Pro Ala Glu Ala Thr Asn Pro Ile Ala Ala Ala Ile 28497 . 1155 1165 1160 28499 Gly Lys Gly Asn Glu Asp Gly Ala Asp Phe Gly Lys Asp Glu Met Lys 28500 1170 1175 1180 28502 Lys Asp Asp Gln Ile Ala Ala Ile Ala Leu Arg Gly Met Ala Lys E--> 28503 185 / 1190 1195 28505 Asp Gly Lys Phe Ala Val Lys Ser Asn Asp Gly Glu Lys Gly Lys Ala 28506 1205 1210 28508 Glu Gly Ala Ile Lys Glu Val Ser Glu Leu Leu Asp Lys Leu Val Lys 1220 1225 1230 28511 Ala Val Lys Thr Ala Glu Gly Ala Ser Ser Gly Thr Asp Ala Ile Gly 28512 1235 1240 1245 28514 Glu Val Val Ala Asn Ala Gly Ala Ala Lys Ala Ala Asp Lys Ala Ser 28515 1250 1255 28517 Val Thr Gly Ile Ala Lys Gly Ile Lys Glu Ile Val Glu Ala Ala Gly E--> 2851 ( 265 )1270 1275 28520 G17 Ser Lys Lys Leu Lys Ala Ala Ala Glu Gly Glu Asn Asn Lys 1285 1290 1295 28523 Lys Ala Gly Lys Leu Phe Gly Lys Ala Gly Ala Gly Ala Gly Ala Asn 28524 1300 1305 1310 28526 Gly Asp Ser Glu Ala Ala Ser Lys Ala Ala Gly Ala Val Ser Ala Gly 1320 1325 28527 1315 33173 <210> SEQ ID NO: 755 33174 <211> LENGTH: 123 est segure in file 33175 <212> TYPE: PRT 33176 <213> ORGANISM: Homo sapiens 33178 <400> SEQUENCE: 755 33179 Cys Asn Ser Asn Asp Thr Asn Asn Ser Gln Thr Lys Ser Arg Gln Lys 5 10 33182 Arg Asp Leu Thr Gln Lys Glu Ala Thr Gln Glu Lys Pro Lys Ser Lys 25 30 20 33185 Glu Glu Leu Leu Arg Glu Lys Leu Asn Asp Asn Gln Lys Thr His Leu



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,230

DATE: 05/08/2001 TIME: 12:00:37

Input Set : N:\COPIES\EBONY\PB481USsl.txt Output Set: N:\CRF3\05082001\I830230.raw

33188 Asp Trp Leu Lys Glu Ala Leu Gly Asn Asp Gly Glu Phe Asn Lys Phe 50 55 60 33191 Leu Gly Tyr Asp Glu Ser Lys Ile Lys Ser Ala Leu Asp His Ile Lys 33192 65 70 75 33194 Ser Glu Leu Asp Ser Cys Thr Gly Asp Lys Val Glu Asn Lys Asn Thr 85 33195 33197 Phe Lys Gln Val Val Gln Glu Ala Leu Lys Gly Gly Ile Asp Gly Phe 100 105 33198 33200 Glu Asn Thr Ala Ser Ser Thr Cys Lys Asn Ser 33201 115 120

E--> 33204

E--> 3320 1

## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



VERIFICATION SUMMARY DATE: 05/08/2001 PATENT APPLICATION: US/09/830,230 TIME: 12:00:38

```
L:8 M:270 C: Current Application Number differs, Replaced Current Application Number
L:464 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:686 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:4889 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103 L:4894 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103 L:4899 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
L:4904 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
L:4909 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
L:4914 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
L:4919 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
L:4924 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
L:4929 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
L:4934 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
L:4939 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
L:4944 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
L:4949 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103 L:4954 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103 L:4959 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:103
\texttt{L:4964~M:341~W:} (46) "n" or "Xaa" used, for SEQ ID#:103
L:4964 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:23 L:4965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103
L:4965 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:24
L:4966 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103
L:4966 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:24
L:4967 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103
L:4967 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:14152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:320
L:14164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:320
L\!:\!14182~M\!:\!341~W\!: (46) "n" or "Xaa" used, for SEQ ID#:320
L:14240 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:320
M:332 Repeated in SeqNo=320
L:14377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:321 L:14389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:321 L:14407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:321
L:14471 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:321
L:16472 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:364
L:18831 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:412
M:332 Repeated in SeqNo=412
L:19119 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:413
M:332 Repeated in SeqNo=413
L:24210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:544
L\!:\!24314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:545
\tt L\!:\!25188~M\!:\!341~W\!: (46) "n" or "Xaa" used, for SEQ ID#:560
L:25253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:561
L:28080\ M:257\ W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:628
L:28085 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:628
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VERIFICATION SUMMARY DATE: 05/08/2001 PATENT APPLICATION: US/09/830,230 TIME: 12:00:38

Input Set : N:\COPIES\EBONY\PB481USs1.txt
Output Set: N:\CRF3\05082001\I830230.raw

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L:28090 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:628
L:28095 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:628
L:28100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:628
L:28105 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:628
L:28110 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:628
L:28115 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:628
L\!:\!28138~M\!:\!341~W\!: (46) "n" or "Xaa" used, for SEQ ID#:628
L:28139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:628
L:28140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:628
L:28194 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:629
L:28199 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:629 L:28204 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:629
L:28209 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:629
L:28214 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:629
L:28219 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:629
L:28224 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:629
L:28229 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:629
L:28239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:629
L:28240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:629
L:28241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:629
L:28349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:630
L\!:\!28355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:630
L:28473 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:630
M:332 Repeated in SeqNo=630
L:28586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:631
L:28592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:631
L:29676 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:664
L:29681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:664
L:29715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:666
L:29971 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:672
L:29976 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:672
L:29989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:672
L:30051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:674
L:30093 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:676
L:30098 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:676
L:30103\ M:257\ W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:676
L:30108 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:676 L:30113 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:676 L:30118 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:676
L:30148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:676
L:30149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:676
L:30295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:678
L:30298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:678
L:30301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:678
L:32231 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:732
L:32250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:732
L:32264 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:733
L\!:\!32280~M\!:\!341~W\!: (46) "n" or "Xaa" used, for SEQ ID#:733
L:32353 \ M:341 \ W: \ (46) \ "n" \ or "Xaa" \ used, for SEQ ID#:734
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5/8/01



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/830,230

DATE: 05/08/2001 TIME: 12:00:38

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L:32430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:735
L:32554 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:740
L:32559 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:740
L:32564 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:740
L:32569 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:740
L:32578\ M:341\ W:\ (46)\ "n"\ or\ "Xaa"\ used, for SEQ\ ID#:740
L:32591\ M:257\ W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:741
L:32596 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:741
L:32601 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:741
L:32606 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:741
L:32614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:741
L:32656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:742
L:32707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:743
L:32710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:743
L:32773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:744
L:32778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:744
L:32779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:744
L:32826 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:745
L:32831 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:745
L:32832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:745
L\colon\!32894 M\colon\!341 W\colon (46) "n" or "Xaa" used, for SEQ ID#:746
L:32915 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:746
L:33204 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:755
M:332 Repeated in SeqNo=755
L:26 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (148) Counted (755)
```